

Jun 12 15:15:52 2001

GenCore version 4.5
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protein - protein search, using sw model

June 12, 2001, 08:16:48 ; Search time 30.76 Seconds

(without alignments)
390.887 Million cell updates/sec

US-09-452-244-10
Effect score: 1893
Sequence: 1 MATTOSQSSSSACSKAAC.....GFSEITDFALEIRKQ 351

BLAST62
Gapop 10.0, Gapext 0.5

93435 seqs, 34255486 residues

93435

DB seq length: 0
DB seq length: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match	Length	ID	Description
1	386.5	20.4	421	1	MTB2_PHYPA
2	377.5	19.9	399	1	MTB2_PHYPA
3	374.5	19.8	228	1	GIL_MART
4	374.5	19.8	255	1	MTB3_MART
5	370.5	19.6	267	1	MTB3_HORVU
6	358	18.9	302	1	MTB3_HORVU
7	358	18.9	340	1	MTB3_MART
8	348.5	18.4	273	1	MTB3_MART
9	340	18.0	252	1	MTB3_MART
10	290.5	15.3	728	1	MTB3_MART
11	274.5	14.5	382	1	MTB3_MART
12	274.5	14.5	624	1	MTB3_MART
13	274.5	14.5	751	1	MTB3_MART
14	270.5	14.3	752	1	MTB3_MART
15	266	14.1	640	1	MTB3_MART
16	265.5	14.0	636	1	MTB3_MART
17	265.5	14.0	640	1	MTB3_MART
18	265.5	14.0	641	1	MTB3_MART
19	265.5	14.0	641	1	MTB3_MART
20	259.5	13.7	657	1	MTB3_MART
21	250.5	13.2	686	1	MTB3_MART
22	250.5	13.2	743	1	MTB3_MART
23	249	13.2	704	1	MTB3_MART
24	242	12.8	700	1	MTB3_MART
25	242	12.8	451	1	MTB3_MART
26	142.5	7.5	757	1	MTB3_MART
27	128	6.8	449	1	MTB3_MART
28	127.5	6.7	810	1	MTB3_MART
29	127.5	6.7	811	1	MTB3_MART
30	114.5	6.0	590	1	MTB3_MART
31	113.5	6.0	595	1	MTB3_MART
32	107.5	5.7	2517	1	MTB3_MART
33	102.5	5.4	562	1	MTB3_MART

34	98.5	5.2	2472	1	NCR2_MOUSE
35	98	5.2	378	1	HAIR_DROVI
36	98	5.2	606	1	HMID_DROAN
37	97.5	5.2	491	1	IRF3_CHICK
38	97	5.1	1169	1	SVF3_DROME
39	95.5	5.0	677	1	DBP1_XENLA
40	95	5.0	1597	1	SOL_DROME
41	94	5.0	1723	1	AIM1_HUMAN
42	93	4.9	753	1	TKR_DROME
43	93	4.9	1039	1	AG43_ECOLI
44	92.5	4.9	515	1	Y141_HUMAN
45	92	4.9	665	1	LAMA_MOUSE

ALIGNMENTS

RESULT 1
ID MTB2_PHYPA STANDARD; PRT; 421 AA.
AC P80073;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE MTB-RELATED PROTEIN PP2.
GN PP2.
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
OC Funariidae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]
RP MEDLINE=94004988; PubMed=8401607;
RA Leach M.J., Kammerer W., Cove D.J., Martin C., Wang T.L.;
RT Expression of myd-related genes in the moss, Physcomitrella patens.";
RL Plant J. 3:51-61(1993).
CC -1- FUNCTION: POSSIBLE TRANSCRIPTION ACTIVATOR.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -1- DEVELOPMENTAL STAGE: HIGH RATES OF GROWTH.
CC -1- SIMILARITY: BELONGS TO THE MYB FAMILY.

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DR EMBL: X67050; CAA47435.1;
DR PIR: S24244; S24244.
DR HSSP: P01103; IPOM.
DR InterPro: IPR001005;
DR Pfam: PF00249; myb.DNA-binding; 2.
DR PROSITE: PS00037; MYB_1; 1.
DR PROSITE: PS00334; MYB_2; 1.
DR PROSITE: PS00900; MYB_3; 2.
KW Nuclear protein; DNA-binding; Repeat; Transcription regulation.
FT DNA BIND 9 61 MYB.
FT DNASIS 62 102 MYB.
SQ SEQUENCE 421 AA; 46695 MW; 27A357857BD0F3F4 CRC64;

Query Match 20.4% Score 386.5; DB 1; Length 421;
Best Local Similarity 21.4% Pred. No. 7.7e-24;
Matches 76; Conservative 16; Mismatches 43; Indels - 13; Gaps 1;

QY 52 KPELRGPTWVDEDLVNTIADNGEGRNMLARAAGLKRGTGSCRLWNTLAPYKRG 111
Dy 9 KVGIRGPTWVDEDLVNTIADNGEGRNMLARAAGLKRGTGSCRLWNTLAPYKRG 68
QY 112 NFSADELLLDLITKGNKWSKIAOHLPGRTNEIKNWTNVQGBAQLNCDANSKRP 171

Applicator

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Db      69  IFSEAEENITLDLHATLNLNRSRSLAALPRTDNENIKYWNTELUKKRLRSQIDPNT--- 126
Oy      172  KQAMRTLMPLHADVDYDITLAAANODDED 199
          || * : : || : |
Db      126  -----HLPLEDSKIDDTEDDTDD 143

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RESULT 2
MYBP MATZEE

ID	MTBP_MAIZE	STANDARD:	PRT:	399 AA.
DT	P27698:			
DT	01-AUG-1992	(Rel. 23, Created)		
DT	01-AUG-1992	(Rel. 23, Last sequence update)		
DT	15-JUL-1999	(Rel. 38, Last annotation update)		
DE	MTB-RELATED PROTEIN P.			
DE	P.			
OS	Zea mays (Maize).			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.			
GN	NCBI_TaxId=4577;			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE-9127138; PubMed-2052342;			
RT	Grotewold E., Altma P., Peterson T.;			
RT	"Alternatively spliced products of the maize P gene encode proteins with homology to the DNA-binding domain of myb-like transcription factors.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 88:4587-4591(1991).			
CC	[2]			
CC	SEQUENCE FROM N.A.			
CC	MEDLINE-92275319; PubMed-1317315;			
CC	Altma P., Grotewold E., Peterson T.;			
CC	"Insertional mutagenesis of the maize P gene by intragenic transposition of Ac.";			
CC	Genetics 131:199-209(1992).			
CC	-1- FUNCTION: TRANSCRIPTION FACTOR POSTULATED TO REGULATE THE BIOSYNTHETIC PATHWAY OF A FLAVONOID-DERIVED PIGMENT IN CERTAIN FLORAL TISSUES.			
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	-1- SIMILARITY: BELONGS TO THE MYB FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sdb.ch/announce/ or send an email to license@isb-sdb.ch)			
CC	EMBL; M73028; AAA33500.1; -			
CC	EMBL; M73029; AAA33501.1; -			
CC	EMBL; Z11879; CAA77939.1; -			
CC	PIR; A39697; A39697.			
CC	PIR; B39697; B39697.			
CC	PIR; S26150; S26150.			
CC	BSSP; P01103; IPOM.			
CC	TRANSFAC; T01590; -			
CC	TRANSFAC; T01591; -			
CC	MaizeDB; 69180; -			
CC	MaizeDB; 69181; -			
CC	InterPro; IPR001005; -			
CC	Pfam; PF00248; myb_DNA-binding; 2.			
CC	PROSITE; PS00037; MYB_1; 1.			
CC	PROSITE; PS00334; MYB_2; 1.			
CC	PROSITE; PS50090; MYB_3; 2.			
CC	Nuclear protein; DNA-binding; Repeat; Transcription regulation; Alternative splicing.			
CC	FT DNA_BIND 9 61 MTB.			
CC	FT DNA_BIND 62 102 MTB.			
CC	FT DOMAIN 178 181 POLY-ALA.			
CC	DOMAIN 305 311 POLY-LEU.			

FT	VARSP.LIC	89	152	WLLTASHLPGSTNDIEITNNVNSHLSQIETRYRRKATGAPD
FT				TALTAIDMSKLSADRRRGCTGP -> RLHATEADYSPSPST
FT				VACLPFGALAVLTLPQSPFPTARITTDIGSALLSVRC
FT	VARSP.LIC	153	399	FACVPSRW (IN SHORT ISOFORM).
FT				MISSING (IN SHORT ISOFORM).
SO	SEQUENCE	399 AA;	43756 MW;	EE025800A44CF5D0 CRC64;

Query Match	19.9%	Score 377.5	DB 1	Length 399
Best Local Similarity	34.8%	Pred. No. 3.8e-23		
Matches 95; Conservative	29	Mismatches 92	Indels 57	Gaps 7

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OY      52 KPEIIRPGPTVDEEDTLVNTJADGSEBNNMLPAAGLKRKSGCRSLWMLYPDPVRG 111
         | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db       9 KYGLJKRGMTAEEDQLNANTAEHGEBSWMSLPKNNGILLRCSCRLWIMYLBADYKRG 68

OY      112 NFSADOLLILDLFTRMGNRNSIAQOLPRTNETENKTWTFRVQKNAQLNCANSKRF 171
         | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db       69 NIKREEDIITILMNTLGNRRSLSLASLPRTDNEIKNTWNS----- 110

OY      172 KDAMRLMPHLADVDYDTA---ANANDDEDHHNHRLYLALHNHO-----AQ 215
         | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db       111 -----ELSRDIETRYRKRYTNGPDVALAIIDSKSQSDRRKRGTRCPRPKASAS 160
         | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY      216 HLOOA-ANAAGGAANDLAAGATDYROLHAL-----PSSMAATSSSOSIASESTD-DGG 267
         | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db       161 RTKDADDDOPGGGAGAPGAPAAASPSHSVDVNPAGEBNSSSGSTGTAEBCGPSSEDAASGP 220
         | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY      268 LLEFANLRAGENCLMDGGDMNAQOEADOGSLMPPPP 300
         | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db       221 WYLEPIRELGDLY-----WGADSEMDALMPGP 248

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RESULT

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ID  GL1_ARATH STANDARD: FRF: 228 AA.
AC  P27900:
DR  01-AUG-1992 (Rel. 23, Created)
DT  01-AUG-1992 (Rel. 23, Last sequence update)
DE  01-OCT-1996 (Rel. 34, Last annotation update)
DE  TRICHOME DIFFERENTIATION PROTEIN GL1.
GN  GL1.
OS  Arabidopsis thaliana (Mouse-ear cress).
OC  Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC  Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC  Brassicales; Brassicaceae; Arabidopsids.
OC  NCBI_TaxID=3702;
RN  (1)
RP  SEQUENCE FROM N.A.
RX  MEDLINE=92034971; PubMed=1934056;
RA  Opdenheimer D.G., Herman P.L., Sivakumaran S., Esch J., Marks M.D.;
RT  "A myb gene required for leaf trichome differentiation in Arabidopsis
RT  is expressed in stipules.";
RL  Cell 67:483-493(1991).
CC  -1- FUNCTION: REGULATES THE PRODUCTION OF A SIGNAL THAT INDUCES
CC  HAIR (TRICHOME) PRECURSOR CELLS ON LEAF PRIMORDIA TO
CC  DIFFERENTIATE.
CC  -1- SIMILARITY: BELONGS TO THE MYB FAMILY.
CC  -----
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CC  -----
DR  EMBL: M73448; AAC97387.1; -.
DR  PIR: A39289; TYWUG1.
DR  HSSP: P01103; 1POM.
DR  TRASNFRAC: T01586; -.
DR  InterPro: IPR001005; -.
DR  Pfam: PF00249; myb_DNA-binding; 2.

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